Please delete the last seven lines of text added to Table I in an amendment to a previous application 07/770,742 in the Response dated September 10, 1992.

In the claims:

Claim 18, line 3, please change "8.5 °C" to -- 8.3 °C --.

Claim 19, line 3, please change "4.5 °C" to -- 4.4 °C --.

~~21.~~ (amended) A method for simultaneously detecting known deletions from at least three DNA sequences, comprising the steps of:

treating said DNA to form single-stranded complementary strands;

adding at least three pairs of oligonucleotide primers, each pair specific for a different sequence, one primer of each pair substantially complementary to a part of the sequence in the sense-strand and the other primer of each pair substantially complementary to a different part of the same sequence in the complementary anti-sense strand and each primer having a Tm such that the lowest Tm and highest Tm of all added primers varies by no more than [8.5] 8.3 °C;

annealing the at least three pairs of primers to their complementary sequences, all primers being subjected to the same reaction conditions;

simultaneously extending said at least three pairs of annealed primers from each primer's 3′ terminus to synthesize an extension product complementary to the strands annealed to each primer, said extension products, after separation from their complement, being capable of serving as templates for the synthesis of an extension product from the other primer of each pair;

separating said extension products from said templates to produce single-stranded molecules;

amplifying said single stranded molecules by repeating, at least once, said annealing, extending and separating steps; and

identifying said amplified extension products from each different sequence; and

analyzing said amplified extension products to detect known deletions.

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22. (amended) A method for simultaneously detecting a presence or absence of at least three target DNA sequences, comprising the steps of:

adding to a common reaction vessel containing a sample mixture of at least three distinct, target sequences in single-stranded form, at least three pairs of oligonucleotide primers, each pair specific for a different sequence, one primer of each pair substantially complementary to a part of the sequence in the sense-strand and the other primer of each pair substantially complementary to a different part of the same sequence in the complementary anti-sense strand and each primer having a Tm such that the lowest Tm and highest Tm of all added primers varies by no more than [8.5] 8.3 °C;

annealing the at least three paris of primers to their complementary sequences, all primers being subject to the same reaction conditions;

simultaneously extending said at least three pairs of annealed primers from each primer's 3' terminus to synthesize an extension product complementary to the strands annealed to each primer, said extension products, after separation from their complement, being capable of serving as templates for the synthesis of an extension product from the other primer of each pair;

separating said extension products from said templates to produce single-stranded molecules;

amplifying said single stranded target sequences by repeating, at least once, said annealing, extending and separating steps; and

identifying whether amplified extension products have been synthesized from each different target sequence, wherein a presence of an extension product indicates the presence of a target sequence and an absence of an extension

product indicates the absence of a target sequence [as a result of the presence or absence of each target sequence].

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~~23.~~ (amended) A method for simultaneously detecting known deletions from at least three DNA sequences, comprising the steps of:

treating said DNA to form single-stranded complementary strands;

adding at least three pairs of oligonucleotide primers, each pair specific for a different sequence, one primer of each pair substantially complementary to a part of the sequence in the sense-strand and the other primer of each pair substantially complementary to a different part of the same sequence in the complementary anti-sense strand and each primer having a Tm such that the lowest Tm and highest Tm of all added primers varies by no more than [4.5] 4.4 °C;

annealing the at least three pairs of primers to their complementary sequences, all primers being subjected to the same reaction conditions;

simultaneously extending said at least three pairs of annealed primers from each primer's 3′ terminus to synthesize an extension product complementary to the strands annealed to each primer, said extension products, after separation from their complement, being capable of serving as templates for the synthesis of an extension product from the other primer of each pair;

separating said extension products from said templates to produce single-stranded molecules;

amplifying said single stranded molecules by repeating, at least once, said annealing, extending and separating steps; and

identifying said amplified extension products from each different sequence; and

analyzing said amplified extension products to detect known deletions.

24. A method for simultaneously detecting at least three target DNA sequences, comprising the steps of:

adding to a common reaction vessel containing a sample mixture of at least three distinct, target sequences in single-stranded form, at least three pairs of oligonucleotide primers, each pair specific for a different sequence, one primer of each pair substantially complementary to a part of the sequence in the sense-strand and the other primer of each pair substantially complementary to a different part of the same sequence in the complementary anti-sense strand and each primer having a Tm such that the lowest Tm and highest Tm of all added primers varies by no more than [4.5] 4.4 °C;

annealing the at least three paris of primers to their complementary sequences, all primers being subject to the same reaction conditions;

simultaneously extending said at least three pairs of annealed primers from each primer's 3' terminus to synthesize an extension product complementary to the strands annealed to each primer, said extension products, after separation from their complement, being capable of serving as templates for the synthesis of an extension product from the other primer of each pair;

separating said extension products from said templates to produce single-stranded molecules;

amplifying said single stranded target sequences by repeating, at least once, said annealing, extending and separating steps; and

identifying whether amplified extension products have been synthesized from each different target sequence, wherein a presence of an extension product indicates the presence of a target sequence and an absence of an extension product indicates the absence of a target sequence [as a result of the presence or absence of each target sequence].

REMARKS

Applicants provide this Response to address the Examiner's Office Action of April 4, 1995. The Applicants thank the Examiner for his consideration and thorough